

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/547,849
Source: IFWP
Date Processed by STIC: 11/3/06

ENTERED



IFWP

RAW SEQUENCE LISTING DATE: 11/03/2006
PATENT APPLICATION: US/10/547, 849 **TIME:** 10:24:54

Input Set : A:\PROL-P01-040.TXT
Output Set: N:\CRF4\11032006\J547849.raw

4 <110> APPLICANT: Reiss, Yuval
5 Taglight, Daniel N.
6 Alroy, Iris
7 Tuvia, Shmuel
8 Barr, Haim Michael
11 <120> TITLE OF INVENTION: CBL-B POLYPEPTIDES, COMPLEXES AND
12 RELATED METHODS
14 <130> FILE REFERENCE: PROL-P01-040
16 <140> CURRENT APPLICATION NUMBER: US 10/547,849

C--> 17 <141> CURRENT FILING DATE: 2005-09-02
19 <150> PRIOR APPLICATION NUMBER: US 60/452,284
20 <151> PRIOR FILING DATE: 2003-03-05
22 <150> PRIOR APPLICATION NUMBER: US 60/456,640
23 <151> PRIOR FILING DATE: 2003-03-20
25 <150> PRIOR APPLICATION NUMBER: US 60/469,462
26 <151> PRIOR FILING DATE: 2003-05-09
28 <150> PRIOR APPLICATION NUMBER: US 60/471,378
29 <151> PRIOR FILING DATE: 2003-05-15
31 <150> PRIOR APPLICATION NUMBER: US 60/480,376
32 <151> PRIOR FILING DATE: 2003-06-19
34 <150> PRIOR APPLICATION NUMBER: US 60/480,215
35 <151> PRIOR FILING DATE: 2003-06-19
37 <160> NUMBER OF SEQ ID NOS: 64
39 <170> SOFTWARE: FastSEQ for Windows Version 4.0
41 <210> SEQ ID NO: 1
42 <211> LENGTH: 2667
43 <212> TYPE: DNA
44 <213> ORGANISM: Homo sapiens
46 <400> SEQUENCE: 1
47 atggatgaat cagccttgtt ggatctttg gagtgtccgg ttgtgtctaga ggcgcatttat 60
48 gcttctgcga aggtcttgcc ttgccagcat acgttttgc aagcatgttt gctggggatc 120
49 gtaggttctc gaaaatgaact cagatgtccc gagtgccaggaa ctcttggatgg 180
50 gaggagcttc ccagtaacat cttgtggc agacttctgg atggcatcaa acagaggcct 240
51 tggaaacctg gtcttgggg gggaaatgggg accaactgca caaatgcatt aagggtctcag 300
52 agcagcactg tggcttaattt tagctcaaaa gatctgcaga gctcccagg 360
53 cctcggtgc aatcctggag cccccactgtg aggggtatac ctcagttacc atgtgc 420
54 gcgttataaca actatgaagg aaaagagcct ggagaccta aattcagcaa aggcgcacatc 480
55 atcattttgc gaagacaagt ggataaaaat tggtaccatg gggaaatgcata 540
56 ggcttttcc ccaccaactt tgtcagatt attaaaccgt tacctcagcc cccacccatc 600
57 tgcaaagcac ttatgactt tgaagtggaaa gacaaggaaag cagacaaaga ttgccttcca 660
58 ttgcggaaagg atgatgttct gactgtgatc cgaagagtttgg atgaaaactg ggctgaagga 720
59 atgctggcag acaaaaatagg aatatttcca atttcatatg ttgagttaa ctcggctgtct 780
60 aaqcaqctqa taqaatqqqa taaqcctcct qtqcccaaggat ttgatgttcc 840

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61 tcggcagcag cccagagcag cactgcccc aagcactccg acaccaagaa gaacaccaaa 900
 62 aaggcgact ctttcaacttc cttcaactatg gccaacaagt cttccaggc atccagaac 960
 63 cggcactcca tggagatcg ccccccgtc ctcatcagct ccagcaaccc cactgctgct 1020
 64 gcacggatca gcgagctgtc tgggctctcc tgcagtgcggc ttctcaggt tcataatagt 1080
 65 accaccgggt taattgtgac cccggcccca agcagccag tgacaactgg cccctcggtt 1140
 66 acttccat cagatgttcc ctaccaagct gcccttgaa ctttgaatcc tcctttcca 1200
 67 ccacccctc tcctggctgc cactgtcctt gcctccacac caccaggcgc caccggcc 1260
 68 gctgctgctg ctggaatggg accgaggccc atggcaggat ccactgacca gattgcacat 1320
 69 ttacggccgc agactcgccc cagtgtgtat gttgtatat atccatacac tcctcgaaa 1380
 70 gaggatgaac tagagcttag aaaaggggag atgttttag tggtagcgg ctgcaggat 1440
 71 ggctggttca aagggacatc catgcatacc agcaagatag gggtttccc tggcaattat 1500
 72 gtggcaccag tcacaagggc ggtgacaaaat gttcccaag etaaagtccc tatgtctaca 1560
 73 gctggccaga caagtcgggg agtgaccatg gtcagtcctt ccacggcagg agggctgcc 1620
 74 cagaagctcc agggaaatgg cgtggctggg agtcccagtg ttgtccccgc agctgtggta 1680
 75 tcagcagctc acatccagac aagtccctcg gctaaggctt tggtagcact gacggggcaa 1740
 76 atgacagtca accaggccc caatgtgtg aggacagttt cagcgcacaa ccagaacgc 1800
 77 cccacggcag cagtgcacacc catccaggtt cagaatgccg ccggcctcaag ccctgcac 1860
 78 gtgggcctgt cccatcaactc gctggcctcc ccacaacctg cgcctctgtt gcaaggctca 1920
 79 gccacgcaca ctgctgccc cagtatcagt cgaggcagtg cccctctggc ctgtgcagca 1980
 80 gctgctccac tgacttcccc aagcatcacc agtgccttc tggaggctga gcccagtggc 2040
 81 cggatagtga ccgttctccc tggactcccc acatctcctg acagtgcctt atcagcttgt 2100
 82 gggAACAGTT cagcaaccaa accagacaag gatagcaaaa aaaaaaaaaa gggtttgg 2160
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 88 cctgtcttga atgagtctag acctgtcggt tggaaaggc acagggtggt ggttccttat 2520
 89 cccctcaga gtgaggcaga acttgaact aaagaaggag atattgtgtt tggcataaaa 2580
 90 aaacgagagg atggctgggtt caaaggcaca ttacaacgtt atggaaaaac tggcctttc 2640
 91 ccaggaagct ttgtggaaaaa catatga 2667
 93 <210> SEQ'ID NO: 2
 94 <211> LENGTH: 888
 95 <212> TYPE: PRT
 96 <213> ORGANISM: Homo sapiens
 98 <400> SEQUENCE: 2
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 100 1 5 10 15
 101 Glu Arg Leu Asp Ala Ser Ala Lys Val Leu Pro Cys Gln His Thr Phe
 102 20 25 30
 103 Cys Lys Arg Cys Leu Leu Gly Ile Val Gly Ser Arg Asn Glu Leu Arg
 104 35 40 45
 105 Cys Pro Glu Cys Arg Thr Leu Val Gly Ser Gly Val Glu Glu Leu Pro
 106 50 55 60
 107 Ser Asn Ile Leu Leu Val Arg Leu Leu Asp Gly Ile Lys Gln Arg Pro
 108 65 70 75 80
 109 Trp Lys Pro Gly Pro Gly Gly Ser Gly Thr Asn Cys Thr Asn Ala
 110 85 90 95
 111 Leu Arg Ser Gln Ser Ser Thr Val Ala Asn Cys Ser Ser Lys Asp Leu

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112	100	105	110
113	Gln Ser Ser Gln Gly Gly Gln Pro Arg Val Gln Ser Trp Ser Pro		
114	115	120	125
115	Pro Val Arg Gly Ile Pro Gln Leu Pro Cys Ala Lys Ala Leu Tyr Asn		
116	130	135	140
117	Tyr Glu Gly Lys Glu Pro Gly Asp Leu Lys Phe Ser Lys Gly Asp Ile		
118	145	150	155
119	Ile Ile Leu Arg Arg Gln Val Asp Glu Asn Trp Tyr His Gly Glu Val		
120	165	170	175
121	Asn Gly Ile His Gly Phe Phe Pro Thr Asn Phe Val Gln Ile Ile Lys		
122	180	185	190
123	Pro Leu Pro Gln Pro Pro Gln Cys Lys Ala Leu Tyr Asp Phe Glu		
124	195	200	205
125	Val Lys Asp Lys Glu Ala Asp Lys Asp Cys Leu Pro Phe Ala Lys Asp		
126	210	215	220
127	Asp Val Leu Thr Val Ile Arg Arg Val Asp Glu Asn Trp Ala Glu Gly		
128	225	230	235
129	Met Leu Ala Asp Lys Ile Gly Ile Phe Pro Ile Ser Tyr Val Glu Phe		
130	245	250	255
131	Asn Ser Ala Ala Lys Gln Leu Ile Glu Trp Asp Lys Pro Pro Val Pro		
132	260	265	270
133	Gly Val Asp Ala Gly Glu Cys Ser Ser Ala Ala Gln Ser Ser Thr		
134	275	280	285
135	Ala Pro Lys His Ser Asp Thr Lys Lys Asn Thr Lys Lys Arg His Ser		
136	290	295	300
137	Phe Thr Ser Leu Thr Met Ala Asn Lys Ser Ser Gln Ala Ser Gln Asn		
138	305	310	315
139	Arg His Ser Met Glu Ile Ser Pro Pro Val Leu Ile Ser Ser Ser Asn		
140	325	330	335
141	Pro Thr Ala Ala Ala Arg Ile Ser Glu Leu Ser Gly Leu Ser Cys Ser		
142	340	345	350
143	Ala Pro Ser Gln Val His Ile Ser Thr Thr Gly Leu Ile Val Thr Pro		
144	355	360	365
145	Pro Pro Ser Ser Pro Val Thr Thr Gly Pro Ser Phe Thr Phe Pro Ser		
146	370	375	380
147	Asp Val Pro Tyr Gln Ala Ala Leu Gly Thr Leu Asn Pro Pro Leu Pro		
148	385	390	395
149	Pro Pro Pro Leu Leu Ala Ala Thr Val Leu Ala Ser Thr Pro Pro Gly		
150	405	410	415
151	Ala Thr Ala Ala Ala Ala Ala Gly Met Gly Pro Arg Pro Met Ala		
152	420	425	430
153	Gly Ser Thr Asp Gln Ile Ala His Leu Arg Pro Gln Thr Arg Pro Ser		
154	435	440	445
155	Val Tyr Val Ala Ile Tyr Pro Tyr Thr Pro Arg Lys Glu Asp Glu Leu		
156	450	455	460
157	Glu Leu Arg Lys Gly Glu Met Phe Leu Val Phe Glu Arg Cys Gln Asp		
158	465	470	475
159	Gly Trp Phe Lys Gly Thr Ser Met His Thr Ser Lys Ile Gly Val Phe		
160	485	490	495

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161 Pro Gly Asn Tyr Val Ala Pro Val Thr Arg Ala Val Thr Asn Ala Ser
162 500 505 510
163 Gln Ala Lys Val Pro Met Ser Thr Ala Gly Gln Thr Ser Arg Gly Val
164 515 520 525
165 Thr Met Val Ser Pro Ser Thr Ala Gly Gly Pro Ala Gln Lys Leu Gln
166 530 535 540
167 Gly Asn Gly Val Ala Gly Ser Pro Ser Val Val Pro Ala Ala Val Val
168 545 550 555 560
169 Ser Ala Ala His Ile Gln Thr Ser Pro Gln Ala Lys Val Leu Leu His
170 565 570 575
171 Met Thr Gly Gln Met Thr Val Asn Gln Ala Arg Asn Ala Val Arg Thr
172 580 585 590
173 Val Ala Ala His Asn Gln Glu Arg Pro Thr Ala Ala Val Thr Pro Ile
174 595 600 605
175 Gln Val Gln Asn Ala Ala Gly Leu Ser Pro Ala Ser Val Gly Leu Ser
176 610 615 620
177 His His Ser Leu Ala Ser Pro Gln Pro Ala Pro Leu Met Pro Gly Ser
178 625 630 635 640
179 Ala Thr His Thr Ala Ala Ile Ser Ile Ser Arg Ala Ser Ala Pro Leu
180 645 650 655
181 Ala Cys Ala Ala Ala Pro Leu Thr Ser Pro Ser Ile Thr Ser Ala
182 660 665 670
183 Ser Leu Glu Ala Glu Pro Ser Gly Arg Ile Val Thr Val Leu Pro Gly
184 675 680 685
185 Leu Pro Thr Ser Pro Asp Ser Ala Ser Ser Ala Cys Gly Asn Ser Ser
186 690 695 700
187 Ala Thr Lys Pro Asp Lys Asp Ser Lys Lys Glu Lys Lys Gly Leu Leu
188 705 710 715 720
189 Lys Leu Leu Ser Gly Ala Ser Thr Lys Arg Lys Pro Arg Val Ser Pro
190 725 730 735
191 Pro Ala Ser Pro Thr Leu Glu Val Glu Leu Gly Ser Ala Glu Leu Pro
192 740 745 750
193 Leu Gln Gly Ala Val Gly Pro Glu Leu Pro Pro Gly Gly His Gly
194 755 760 765
195 Arg Ala Gly Ser Cys Pro Val Asp Gly Asp Gly Pro Val Thr Thr Ala
196 770 775 780
197 Val Ala Gly Ala Ala Leu Ala Gln Asp Ala Phe His Arg Lys Ala Ser
198 785 790 795 800
199 Ser Leu Asp Ser Ala Val Pro Ile Ala Pro Pro Arg Gln Ala Cys
200 805 810 815
201 Ser Ser Leu Gly Pro Val Leu Asn Glu Ser Arg Pro Val Val Cys Glu
202 820 825 830
203 Arg His Arg Val Val Val Ser Tyr Pro Pro Gln Ser Glu Ala Glu Leu
204 835 840 845
205 Glu Leu Lys Glu Gly Asp Ile Val Phe Val His Lys Lys Arg Glu Asp
206 850 855 860
207 Gly Trp Phe Lys Gly Thr Leu Gln Arg Asn Gly Lys Thr Gly Leu Phe
208 865 870 875 880
209 Pro Gly Ser Phe Val Glu Asn Ile

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210 885
 213 <210> SEQ ID NO: 3
 214 <211> LENGTH: 5128
 215 <212> TYPE: DNA
 216 <213> ORGANISM: Homo sapiens
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 221 gttacatgag tcatttttaag ggtatgcacac aactatgaac atttctgaag atttttctc 180
 222 agtaaaatgtt ataaatggatgg atgaatcaggc cttgttggat cttttggagt gtccgggttg 240
 223 tcttagagcgc cttgtatgctt ctgcgaaggc cttgccttgc cagcatacgt tttgcaagcg 300
 224 atgtttgtcg gggatcgtag ttctcgaaaa tgaactcaga tgcgtccaggc gcaggactct 360
 225 tggtggctcg ggtgtcgagg agttccccag taacatcttgc ctggtcagac ttctggatgg 420
 226 catcaaacag aggccttggaa aacctggtcc tgggtggggaa agtgggacca actgcacaaa 480
 227 tgcatttaagg tctcagagca gcactgtggc taattgttagc tcaaaagatc tgcaagagctc 540
 228 ccaggcgcca cagcagccctc ggggtcaatc ctggagcccc ccagtggagg gtataccctca 600
 229 gttaccatgtt gccaaagcgt tatacaacta tgaaggaaaa gagcctggag accttaaattt 660
 230 cagcaaaggc gacatcatca ttttgcgaag acaagtggat gaaaatttgtt accatgggaa 720
 231 .agtcaatyggc atccatggct ttttccccac caactttgtt cagattatta aaccgttacc 780
 232 tcagccccca ctcgtcgca aagcacttta tgactttgaa gtgaaagaca aggaaggdaga 840
 233 caaagattgc cttccatttgc caaaggatga tggtctgact gtgtccggaa gagtggatga 900
 234 aaactgggtt gaaggaaatgc tggcagacaa aataggaata ttcccaattt catatgttga 960
 235 gtttaactcg gctgctaaggc agctgataga atgggataag cctcctgtgc caggagttga 1020
 236 tgctggagaaa tgttccctgg cagcagccca gagcagcact gccccaaagc actccgacac 1080
 237 caagaagaac accaaaaagc ggcactccctt cactccctc actatggcca acaagtccctc 1140
 238 ccaggcatcc cagaaccgc actccatggc gatcagcccc cctgtccca tcagctccag 1200
 239 caaccccaact gctgctgcac ggatcagcga gctgtctggg ctctcctgca gtgcccccttc 1260
 240 tcaggttcat ataagtacca ccgggttaat tggatccccg ccccaagca gcccagtgac 1320
 241 aactggcccc tcgtttactt tcccatcaga tgttccctac caagctgccc ttggaaacttt 1380
 242 gaatcccttcttcccttcccttggcttccact gtccttgctt ccacaccacc 1440
 243 aggccgcacc gccgcgcgtg ctgctgtgg aatgggacccg aggcccatgg caggatccac 1500
 244 tgaccagatttgc acatatttac ggccgcagac tcgccccagt gtgtatgtt ctatatatcc 1560
 245 atacactcccttcccttcccttggcttccact gtccttgctt ccacaccacc 1560
 246 tgagcgtgc caggatggcttcccttcccttggcttccact gtccttgctt ccacaccacc 1620
 247 ttcccttggc aattatgtgg caccagtccac aaggccgttccact gtccttgctt ccacaccacc 1680
 248 agtccctatgttcccttcccttggcttccact gtccttgctt ccacaccacc 1740
 249 ggcaggaggc cctgcccaga agtcccttccact gtccttgctt ccacaccacc 1800
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 251 gcacatgacggccatgttcccttcccttggcttccact gtccttgctt ccacaccacc 1920
 252 gcacaaccatgttcccttcccttggcttccact gtccttgctt ccacaccacc 1980
 253 cctcggccatgttcccttcccttggcttccact gtccttgctt ccacaccacc 2040
 254 tctgtatgcacccatgttcccttcccttggcttccact gtccttgctt ccacaccacc 2100
 255 tctggccatgttcccttcccttggcttccact gtccttgctt ccacaccacc 2160
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 257 tgcttcatca gcttggggaa acagttccact gtccttgctt ccacaccacc 2280
 258 aaaaaagggtt tggttgaatgttcccttcccttggcttccact gtccttgctt ccacaccacc 2340
 259 tcctccatca tcgccccccatgttcccttcccttggcttccact gtccttgctt ccacaccacc 2400
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 261 ggacggggac ggaccggatca cgactgcgttcccttcccttggcttccact gtccttgctt ccacaccacc 2520
 262 ggacggggac ggaccggatca cgactgcgttcccttcccttggcttccact gtccttgctt ccacaccacc 2580

RAW SEQUENCE LISTING ERROR SUMMARY
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FYI
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:43; N Pos. 4,10,12,13,58,74,136,206,222,237,254,385,1336,1344,1347
Seq#:43; N Pos. 1350,1380,1392,1395,1400,1445

VERIFICATION SUMMARY
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L:17 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:1610 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43 after pos.:0
L:1611 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43 after pos.:60
L:1612 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43 after pos.:120
L:1613 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43 after pos.:180
L:1614 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43 after pos.:240
L:1616 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43 after pos.:360
L:1632 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43 after pos.:1320
L:1633 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43 after pos.:1380
L:1634 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43 after pos.:1440